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Skovgaard, Kerstin; Brogaard, Louise; Heegaard, Peter M. H.; Schou, Kirstine Klitgaard

Publication date:
2014

Document Version
Peer reviewed version

[Link back to DTU Orbit](#)

Citation (APA):
Skovgaard, K., Brogaard, L., Heegaard, P. M. H., & Schou, K. K. (2014). *The pig as a large animal model for characterization of host-pathogen interactions*. Abstract from Immunology and Infectious Diseases, Sandbjerg , Denmark.

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'Immunology and Infectious Diseases' 3-5 September 2014, Sandbjerg Gods

The pig as a large animal model for characterization of host-pathogen interactions

Kerstin Skovgaard, Louise Brogaard, Peter M. H. Heegaard, Kirstine Klitgaard Schou

National Veterinary Institute, Technical University of Denmark

Large animal models are essential in understanding the mechanisms involved in human infectious disease. To study the expression of host and bacterial genes involved in defense and survival mechanisms, we analyzed lung tissue from pigs experimentally infected with the Gram-negative bacterium *A. pleuropneumoniae*. All steps including RNA extraction and high-throughput real-time qPCR were carried out simultaneously for the two organisms. By applying this dual-organism approach, we obtained unique insights into the host-pathogen interaction at the site of infection. Differential expression of host genes involved in innate immune responses towards Gram-negative infections, including pattern recognition receptors and cytokines **concurrent** with expression of bacterial genes involved in lipopolysaccharide biosynthesis and adhesion was demonstrated.

We also studied the gene expression in blood leukocytes after experimental H1N2 virus infection of pigs, and found the regulation of several swine encoded miRNAs and cytokines to mimic key findings from influenza studies in human patients. By employing the pig as a model we were able to perform highly controlled experimental infections and to study changes of symptoms, viral titer, and expression of microRNAs/mRNAs as the influenza infection progressed in time, generating information that would be difficult to obtain from human patients.